SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Communi, Didier
                        Pirotton, Sabine
                        Parmentier, Marc
                        Boeynaems, Jean-Marie

   (ii) TITLE OF INVENTION: RECEPTOR AND NUCLEIC ACID MOLECULE ENCODING SAID RECEPTOR

   (iii) NUMBER OF SEQUENCES: 4

   (iv) CORRESPONDANCE ADDRESS:
      (A) ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
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      (D) STATE OR PROVINCE: California
      (E) COUNTRY: USA
      (F) ZIP: 92101-3505

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

   (vi) CURRENT APPLICATION DATA:
      APPLICATION NUMBER: WO PCT/BE 96/00123

   (vii)   ATTORNEY/AGENT INFORMATION:
      (A) NAME: Bartfeld, Ph.D., Neil
      (B) REGISTRATION NUMBER: 39,901
      (C) REFERENCE/DOCKET NUMBER: VANMA83.001APC

   (viii)   TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: (619) 235-8550
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(2) INFORMATION FOR SEQ ID NO: 1:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1429 base pairs
      (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
    (A) NAME/KEY: CDS
    (B) LOCATION:181..1275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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AAGGGAGCTT  GGGTAGGGGC  CAGGCTAGCC  TGAGTGCACC  CAGATGCGCT
TCTGTCAGCT  60

CTCCCTAGTG  CTTCAACCAC  TGCTCTCCCT  GCTCTACTTT  TTTTGCTCCA
GCTCAGGGAT  120

GGGGGTGGGC  AGGGAAATCC  TGCCACCCTC  ACTTCTCCCC  TTCCCATCTC
CAGGGGGGCC  180
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ATG GCC AGT ACA GAG TCC TCC CTG TTG AGA TCC CTA GGC CTC AGC CCA
    228
Met Ala Ser Thr Glu Ser Ser Leu Leu Arg Ser Leu Gly Leu Ser Pro
 1           5                10               15
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GGT CCT GGC AGC AGT GAG GTG GAG CTG GAC TGT TGG TTT GAT GAG GAT
    276
Gly Pro Gly Ser Ser Glu Val Glu Leu Asp Cys Trp Phe Asp Glu Asp
        20               25               30
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TTC AAG TTC ATC CTG CTG CCT GTG AGC TAT GCA GTT GTC TTT GTG CTG
 324
Phe Lys Phe Ile Leu Leu Pro Val Ser Tyr Ala Val Val Phe Val Leu
     35               40               45
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GGC TTG GGC CTT AAC GCC CCA ACC CTA TGG CTC TTC ATC TTC CGC CTC
 372
Gly Leu Gly Leu Asn Ala Pro Thr Leu Trp Leu Phe Ile Phe Arg Leu
     50               55               60
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CGA CCC TGG GAT GCA ACG GCC ACC TAC ATG TTC CAC CTG GCA TTG TCA
 420
Arg Pro Trp Asp Ala Thr Ala Thr Tyr Met Phe His Leu Ala Leu Ser
65               70               75               80
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GAC ACC TTG TAT GTG CTG TCG CTG CCC ACC CTC ATC TAC TAT TAT GCA
  468
Asp Thr Leu Tyr Val Leu Ser Leu Pro Thr Leu Ile Tyr Tyr Tyr Ala
           85   90   95

GCC CAC AAC CAC TGG CCC TTT GGC ACT GAG ATC TGC AAG TTC GTC CGC
  516
Ala His Asn His Trp Pro Phe Gly Thr Glu Ile Cys Lys Phe Val Arg
          100   105   110

TTT CTT TTC TAT TGG AAC CTC TAC TGC AGT GTC CTT TTC CTC ACC TGC
  564
Phe Leu Phe Tyr Trp Asn Leu Tyr Cys Ser Val Leu Phe Leu Thr Cys
       115   120   125

ATC AGC GTG CAC CGC TAC CTG GGC ATC TGC CAC CCA CTT CGG GCA CTA
  612
Ile Ser Val His Arg Tyr Leu Gly Ile Cys His Pro Leu Arg Ala Leu
  130   135   140

CGC TGG GGC CGC CCT CGC CTC GCA GGC CTT CTC TGC CTG GCA GTT TGG
  660
Arg Trp Gly Arg Pro Arg Leu Ala Gly Leu Leu Cys Leu Ala Val Trp
145   150   155   160

TTG GTC GTA GCC GGC TGC CTC GTG CCC AAC CTG TTC TTT GTC ACA ACC
  708
Leu Val Val Ala Gly Cys Leu Val Pro Asn Leu Phe Phe Val Thr Thr
       165   170   175

AGC AAC AAA GGG ACC ACC GTC CTG TGC CAT GAC ACC ACT CGG CCT GAA
  756
Ser Asn Lys Gly Thr Thr Val Leu Cys His Asp Thr Thr Arg Pro Glu
     180   185   190

GAG TTT GAC CAC TAT GTG CAC TTC AGC TCG GCG GTC ATG GGG CTG CTC
  804
Glu Phe Asp His Tyr Val His Phe Ser Ser Ala Val Met Gly Leu Leu
     195   200   205

TTT GGC GTG CCC TGC CTG GTC ACT CTT GTT TGC TAT GGA CTC ATG GCT
  852
Phe Gly Val Pro Cys Leu Val Thr Leu Val Cys Tyr Gly Leu Met Ala
  210   215   220

CGT CGC CTG TAT CAG CCC TTG CCA GGC TCT GCA CAG TCG TCT TCT CGC

900
Arg Arg Leu Tyr Gln Pro Leu Pro Gly Ser Ala Gln Ser Ser Ser Arg
225   230   235   240

CTC CGC TCT CTC CGC ACC ATA GCT GTG GTG CTG ACT GTC TTT GCT GTC
948
Leu Arg Ser Leu Arg Thr Ile Ala Val Val Leu Thr Val Phe Ala Val
        245   250   255

TGC TTC GTG CCT TTC CAC ATC ACC CGC ACC ATT TAC TAC CTG GCC AGG
996
Cys Phe Val Pro Phe His Ile Thr Arg Thr Ile Tyr Tyr Leu Ala Arg
        260   265   270

CTG TTG GAA GCT GAC TGC CGA GTA CTG AAC ATT GTC AAC GTG GTC TAT
1044
Leu Leu Glu Ala Asp Cys Arg Val Leu Asn Ile Val Asn Val Val Tyr
    275   280   285

AAA GTG ACT CGG CCC CTG GCC AGT GCC AAC AGC TGC CTG GAT CCT GTG
1092
Lys Val Thr Arg Pro Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val
    290   295   300

CTC TAC TTG CTC ACT GGG GAC AAA TAT CGA CGT CAG CTC CGT CAG CTC
1140
Leu Tyr Leu Leu Thr Gly Asp Lys Tyr Arg Arg Gln Leu Arg Gln Leu
305   310   315   320

TGT GGT GGT GGC AAG CCC CAG CCC CGC ACG GCT GCC TCT TCC CTG GCA
1188
Cys Gly Gly Gly Lys Pro Gln Pro Arg Thr Ala Ala Ser Ser Leu Ala
        325   330   335

CTA GTG TCC CTG CCT GAG GAT AGC AGC TGC AGG TGG GCG GCC ACC CCC
1236
Leu Val Ser Leu Pro Glu Asp Ser Ser Cys Arg Trp Ala Ala Thr Pro
        340   345   350

CAG GAC AGT AGC TGC TCT ACT CCT AGG GCA GAT AGA TTC TAACACGGGA
1285
Gln Asp Ser Ser Cys Ser Thr Pro Arg Ala Asp Arg Phe
        355   360   365

AGCCGGCAAG TGAGAGAAAA GGGGATGAGT GCAGGGCAGA GGTGAGGGAA
CCCAATAGTG 1345

ATACCTGGTA AGGTGCTTCT TCCTCTTTTC CAGGCTCTGG AGAGAAGCCC
TCACCCTGAG 1405

GGTTGCCACG GAGGCAGGGA TATC   1429

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 365 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Ser Thr Glu Ser Ser Leu Leu Arg Ser Leu Gly Leu Ser Pro
  1   5   10   15

Gly Pro Gly Ser Ser Glu Val Glu Leu Asp Cys Trp Phe Asp Glu Asp
        20   25   30

Phe Lys Phe Ile Leu Leu Pro Val Ser Tyr Ala Val Val Phe Val Leu
     35   40   45

Gly Leu Gly Leu Asn Ala Pro Thr Leu Trp Leu Phe Ile Phe Arg Leu
    50   55   60

Arg Pro Trp Asp Ala Thr Ala Thr Tyr Met Phe His Leu Ala Leu Ser
 65   70   75   80

Asp Thr Leu Tyr Val Leu Ser Leu Pro Thr Leu Ile Tyr Tyr Tyr Ala
        85   90   95

Ala His Asn His Trp Pro Phe Gly Thr Glu Ile Cys Lys Phe Val Arg
       100   105   110

Phe Leu Phe Tyr Trp Asn Leu Tyr Cys Ser Val Leu Phe Leu Thr Cys
    115   120   125

Ile Ser Val His Arg Tyr Leu Gly Ile Cys His Pro Leu Arg Ala Leu
   130   135   140

Arg Trp Gly Arg Pro Arg Leu Ala Gly Leu Leu Cys Leu Ala Val Trp
145   150   155   160

Leu Val Val Ala Gly Cys Leu Val Pro Asn Leu Phe Phe Val Thr Thr
       165   170   175

Ser Asn Lys Gly Thr Thr Val Leu Cys His Asp Thr Thr Arg Pro Glu
     180   185   190

Glu Phe Asp His Tyr Val His Phe Ser Ser Ala Val Met Gly Leu Leu
     195   200   205

Phe Gly Val Pro Cys Leu Val Thr Leu Val Cys Tyr Gly Leu Met Ala
    210   215   220

Arg Arg Leu Tyr Gln Pro Leu Pro Gly Ser Ala Gln Ser Ser Ser Arg
225   230   235   240

Leu Arg Ser Leu Arg Thr Ile Ala Val Val Leu Thr Val Phe Ala Val
     245   250   255

Cys Phe Val Pro Phe His Ile Thr Arg Thr Ile Tyr Tyr Leu Ala Arg
     260   265   270

Leu Leu Glu Ala Asp Cys Arg Val Leu Asn Ile Val Asn Val Val Tyr
     275   280   285

Lys Val Thr Arg Pro Leu Ala Ser Ala Asn Ser Cys Leu Asp Pro Val
    290   295   300

Leu Tyr Leu Leu Thr Gly Asp Lys Tyr Arg Arg Gln Leu Arg Gln Leu
305   310   315   320

Cys Gly Gly Gly Lys Pro Gln Pro Arg Thr Ala Ala Ser Ser Leu Ala
     325   330   335

Leu Val Ser Leu Pro Glu Asp Ser Ser Cys Arg Trp Ala Ala Thr Pro
     340   345   350

Gln Asp Ser Ser Cys Ser Thr Pro Arg Ala Asp Arg Phe
     355   360   365

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGATCTAGA TACTATGTTC TACACTCTTA CGTGC   35

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 35 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCTTAAGCTT GGAGTCACGT ACGAGCAAGC TAGTT   35